

### REMARKS

Within the specification, Applicants have amended the paragraph beginning at page 79, line 22 to correct a spelling error and to include sequence listing references that were omitted. Substitute paper and electronic copies of the sequence listing are included herewith.

Applicants have amended independent claims 1 and 9 to recite a nucleic acid molecule that comprises a nucleic acid sequence that (a) has the specified percentage identity to SEQ ID NO:62, (b) encodes an amino acid sequence with the specified percentage identity to SEQ ID NO:63, or (c) is fully complementary to the nucleic acid sequence of (a) or (b). Independent claim 15 has been amended to depend from claim 9, and recites a nucleic acid molecule having 100 percent identity to SEQ ID NO:62. All references to non-elected sequences thus have been removed from the claims. In addition, claims 1 and 9 have been amended to contain proper Markush groups and to correct punctuation errors, and claim 25 has been amended to remove the term "etc." Claims 2-3, 10-11, and 16-17 have been amended to refer to transformed seeds and plants containing recombination constructs. Support for these amendments can be found in the specification at, for example, page 38, lines 5-6, and page 42, lines 5-32. Claims 4, 12 and 18 have been amended to depend from new claims 26, 27 and 33, respectively, and now relate to nucleic acid molecules that include gag and env coding sequences. Support for these amendments can be found in original claims 4, 12 and 18.

New dependent claims 26-33 are presented herewith. Claims 26 and 27 relate to pol coding sequences that comprise the nucleic acid molecules of claims 1 and 9, respectively. Support for these new claims can be found in original claims 4 and 12. Claim 28 recites a nucleic acid molecule encoding a polypeptide having an amino acid sequence with 100 percent identity to SEQ ID NO:63. Claims 29 and 30 recite a transformed seed and a transformed plant, respectively, containing a recombination construct comprising the nucleic acid of claim 28. Claim 31 relates to a pol coding sequence comprising the nucleic acid of claim 28, and claim 32 recites that the nucleic acid of claim 31 further comprises gag and env coding sequences. Support for these claims can be found in original claims 15-18. Claim 33 is directed to pol coding sequences that comprise the nucleic acid molecule of claim 15. Support for this claim can be found in original claim 18. No new matter is added by the amendments to the claims and

specification indicated above. Applicants request reconsideration and allowance of claims 1-4, 9-12, 15-18, 21-23, 25, and 26-33 in view of these amendments and the following remarks.

#### Claim Objections

The Examiner objected to claims 1-4, 9-12, 15-18, 21-23 and 25 for containing references to non-elected subject matter. The Examiner also objected to claims 1, 9 and 15 for containing inappropriate punctuation. Applicants have amended independent claims 1, 9 and 15 to refer specifically to SEQ ID NO:62 and SEQ ID NO:63. The punctuation within claims 1, 9 and 15 also has been corrected or removed by amendment. Applicants request that the Examiner withdraw the objection to claims 1-4, 9-12, 15-18, 21-23, and 25.

#### Rejections under 35 U.S.C. § 112, first paragraph

The Examiner rejected claims 1-4, 9-12, 15-18, 21-23 and 25 under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in a manner to convey possession of the invention at the time of filing. Applicants respectfully traverse.

Independent claims 1, 9 and 15 are directed to nucleic acid molecules that have at least 85% identity, at least 95% identity, and 100% identity, respectively, to SEQ ID NO:62. These claims also relate to nucleic acid molecules encoding amino acid sequences having at least 85% identity, at least 95% identity, and 100% identity, respectively, to SEQ ID NO:63. The Examiner asserted that the claims and the specification do not indicate the distinguishing attributes shared by members of this broad genus, nor do they place a limit on the number of alterations that can be made to the claimed nucleic acids. The Examiner further asserted that the specification does not disclose what modifications can be tolerated to maintain the activity of the encoded polypeptide, and does not disclose an example of "a nucleic acid having 85% or 90% [sic] identity encoding a functional retroelement reverse transcriptase." In addition, the Examiner stated that the general knowledge and level of skill in the art do not supplement the description, because specific rather than general guidance is needed as to what changes can be made in the nucleotide sequence.

Applicants respectfully disagree with the Examiner's assertion, because the claims do indicate the shared attributes of the claimed nucleic acids. The genus of nucleic acids either

share the specified percentage identity to the nucleotide sequence set forth in SEQ ID NO:62, or encode polypeptides that share the specified percentage identity to SEQ ID NO:63. Furthermore, the claims and specification do place a limit on the number of changes that can be made to the nucleic acid molecules: claim 1 indicates that no more than a 15% difference in sequence identity can be permitted, while claim 9 indicates that no more than a 5% difference in sequence identity can be permitted. Claim 15 indicates that no difference in sequence identity is permitted.

Claims 1, 9 and 15 have been amended to remove the recitation that the nucleic acid molecule encodes at least a portion of a reverse transcriptase. In light of these amendments, the Examiner's argument concerning modifications that maintain reverse transcriptase activity is moot. The Examiner's assertion that the specification does not disclose a representative example of a nucleic acid having 85% or 95% identity and encoding a functional retroelement reverse transcriptase also is moot. With respect to the Examiner's assertion that specific guidance is required, Applicants submit that specific guidance is provided, i.e., the specification indicates that the sequences set forth in SEQ ID NO:62 and SEQ ID NO:63 are to be used. Specification at page 57, lines 8-16.

The Examiner also rejected claims 1-4, 9-12, 15-18, 21-23 and 25 under 35 U.S.C. § 112, first paragraph, as being non-enabling. The Examiner asserted that the specification failed to teach how to use a nucleic acid encoding at least a portion of a reverse transcriptase. The Examiner assumed that "the portion of the nucleic acid need not be functional nor result in a functional reverse transcriptase." The Examiner also stated that the specification does not disclose "which nucleic acid sequences are functional, how to use the non-functional nucleic acid sequences, which sequences with 85% or 95% homology are active and encode functional reverse transcriptases, and how complementary nucleic acid sequences encode functional reverse transcriptases." The Examiner is correct that the claimed nucleic acids need not result in a functional reverse transcriptase. Thus, these arguments are moot in light of the above claim amendments. In addition, Applicants refer to page 38, lines 18-35, which specifically describe uses of the claimed nucleic acids.

In view of the above remarks, Applicants request that the Examiner withdraw the rejections of claims 1-4, 9-12, 15-18, 21-23 and 25 under 35 U.S.C. § 112, first paragraph.

Rejections under 35 U.S.C. § 112, second paragraph

The Examiner rejected claims 1-4, 9-12, 15-18, 21-23 and 25 under 35 U.S.C. § 112, second paragraph, as being indefinite. The Examiner alleged that in claims 1, 9 and 15, the determination of nucleic acid sequence identity based on the DNAsis computer program renders the claims vague and indefinite because "DNA sequence comparison algorithms are subject to change depending upon the technology available." The Examiner also stated that limitation to a particular algorithm renders the metes and bounds of the claim unclear. Claims 1, 9 and 15 have been amended to delete the recitation that identity can be determined using the indicated computer program and default parameters, thus rendering the rejection moot.

The Examiner also objected to the use of "*etc.*" in claim 25. Applicants have amended claim 25 to remove the term "*etc.*"

The Examiner further objected to the use of improper Markush format in steps (c) and (d) of claims 1, 9 and 15. Amended claims 1 and 9 include an acceptable Markush format. Amended claim 15 does not contain a Markush group. In view of these amendments and remarks, Applicants request that the Examiner withdraw the rejections of claims 1-4, 9-12, 15-18, 21-23 and 25 under 35 U.S.C. § 112, second paragraph.

CONCLUSION

Applicants request reconsideration and allowance of claims 1-4, 9-12, 15-18, 21-23 and 25. Applicants also request reconsideration of the restriction requirement instituted in the Office Action mailed April 8, 2002. The Examiner is invited to telephone the undersigned agent if it is felt that such would advance prosecution of the application.

Attached is a marked-up version of the changes being made by the current amendments. Applicants also have amended the sequence listing to correct the omission of several sequences. Applicants submit herewith a substitute paper copy and computer readable form of the sequence listing in compliance with 37 C.F.R. §§ 1.821-1.825.

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Respectfully submitted,

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**Version with markings to show changes made**

**In the specification:**

The paragraph beginning at page 79, line 22 has been amended as follows:

The degenerate oligos DVO1197 (5' GTG-CGN-AAR-GAR-GTN-NTN-AAR-YT 3' (SEQ ID NO:166) for the N terminal amino acid sequence VRKEVLKL (SEQ ID NO:167)) and DVO1198 (5' AAC-YTT-NGW-RAA-RTC-YTT-DAT-RAA 3' (SEQ ID NO:168) for the C terminal amino acid sequence VKSFDKIF (SEQ ID NO:169)) were used to amplify the Xiong/Eickbush plant retrovirus reverse transcriptase domain from genomic DNA of the following plants: New sequences were obtained from *Nicotiana tabacum* (Tobacco), *Platanus occidentalis* (Sycamore), *Gossypium hirsutum* (Cotton), *Lycopersicon esculentum* (Tomato) *Solanum tuberosum* (Potato), *Oryza sativa* (Rice), *Triticum aestivum* (Wheat), *Hordeum vulgare* (Barley), *Sorghum bicolor* (Sorghum), *Avena sativa* (Oat), *Secale cereale* (Rye). No sequence was obtained from *Pinus coulteri* (Big-cone pine), *Zea mays* (Corn), *Zea mays* subspecies[.] *parviglumis* (Teosinte), and a *Tripsacum* species. A positive control for PCR was used to obtain previously known sequences from: *Arabidopsis thaliana*, *Pisum sativum* (pea) and three varieties (Hark 89, L85 and Williams) of *Glycine max* (soybean).

**In the claims:**

Claims 5-8, 13-14, 19-20 and 24 have been cancelled.

Claims 1-4, 9-12, 15-18, 21-23 and 25 have been amended as follows:

1. (Amended) An isolated nucleic acid molecule[, wherein said nucleic acid molecule encodes at least a portion of a plant retroelement reverse transcriptase and comprises] comprising a [nucleic acid] nucleotide sequence selected from the group consisting of:

(a) a [nucleic acid] sequence having more than 85% identity to [a nucleic acid sequence selected from the group consisting of even-numbered SEQ ID NOs inclusive from SEQ ID NO 42 to SEQ ID NO 164, wherein said identity can be determined using the DNAsis computer program and default parameters] SEQ ID NO 62;

(b) a [nucleic acid] sequence [which encodes] encoding a polypeptide comprising an amino acid sequence having more than 85% identity to [an amino acid sequence selected from the group consisting of odd-numbered SEQ ID NOs inclusive from SEQ ID NO 43 through SEQ ID NO 165, wherein said identity can be determined using the DNAsis computer program and default parameters] SEQ ID NO 63; and

(c) [a nucleic acid sequence which encodes an allelic variant of a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).

(d)] a [nucleic acid] sequence fully complementary to [a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of] (a)[; a nucleic acid sequence of] or (b).

2. (Amended) A transformed seed containing a recombination construct comprising a nucleic acid of claim 1.

3. (Amended) A transformed plant containing a recombination construct comprising a nucleic acid of claim 1.

4. (Amended) [A] The nucleic acid molecule of claim [1, which comprises] 26, said nucleic acid further comprising a gag coding sequence[, pol] and an env [genes and which comprises] coding sequence, wherein adenine-thymidine-guanidine [as] is the gag [gene] coding sequence start codon.

9. (Amended) An isolated nucleic acid molecule[, wherein said nucleic acid molecule encodes at least a portion of a plant retroelement reverse transcriptase and comprises] comprising a [nucleic acid] nucleotide sequence selected from the group consisting of:

(a) a [nucleic acid] sequence having more than 95% identity to [a nucleic acid sequence selected from the group consisting of even-numbered SEQ ID NOs inclusive from SEQ ID NO 42 to SEQ ID NO 164, wherein said identity can be determined using the DNAsis computer program and default parameters] SEQ ID NO 62;

(b) a [nucleic acid] sequence [which encodes] encoding a polypeptide comprising an amino acid sequence having more than 95% identity to [an amino acid sequence selected from

the group consisting of odd-numbered SEQ ID NOs inclusive from SEQ ID NO 43 through SEQ ID NO 165, wherein said identity can be determined using the DNAsis computer program and default parameters] SEQ ID NO 63; and

(c) [a nucleic acid sequence which encodes an allelic variant of a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).

(d)] a [nucleic acid] sequence fully complementary to [a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of] (a)[; a nucleic acid sequence of] or (b).

10. (Amended) A transformed seed containing a recombination construct comprising a nucleic acid of claim 9.

11. (Amended) A transformed plant containing a recombination construct comprising a nucleic acid of claim 9.

12. (Amended) [A] The nucleic acid molecule of claim 9, which comprises] 27, said nucleic acid further comprising a gag coding sequence[, pol] and an env [genes and which comprises] coding sequence, wherein adenine-thymidine-guanidine [as] is the gag [gene] coding sequence start codon.

15. (Amended) [An isolated] The nucleic acid molecule of claim 9, wherein said nucleic acid molecule [encodes at least a portion of a plant retroelement reverse transcriptase and] comprises a nucleic acid sequence [selected from the group consisting of:

(a) a nucleic acid sequence selected from the group consisting of even-numbered SEQ ID NOs inclusive from SEQ ID NO 42 to SEQ ID NO 164, wherein said identity can be determined using the DNAsis computer program and default parameters;

(b) a nucleic acid sequence which encodes an amino acid sequence selected from the group consisting of odd-numbered SEQ ID NOs inclusive from SEQ ID NO 43 through SEQ ID NO 165, wherein said identity can be determined using the DNAsis computer program and default parameters;

(c) a nucleic acid sequence which encodes an allelic variant of a nucleic acid sequence



selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).

(d) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b)] having 100% identity to SEQ ID NO:62.

16. (Amended) A transformed seed containing a recombination construct comprising a nucleic acid of claim 15.

17. (Amended) A transformed plant containing a recombination construct comprising a nucleic acid of claim 15.

18. (Amended) [A] The nucleic acid molecule of claim [15, which comprises] 33, said nucleic acid further comprising a gag coding sequence[, pol] and an env [genes and which comprises] coding sequence, wherein adenine-thymidine-guanidine [as] is the gag [gene] coding sequence start codon.

21. (Amended) [A] The nucleic acid of claim 15, which further comprises at least one nucleic acid sequence which encodes at least one agronomically-significant characteristic.

22. (Amended) [A] The nucleic acid molecule of claim 21, wherein the agronomically-significant characteristic is selected from the group consisting of: male sterility; self-incompatibility; foreign organism resistance; improved biosynthetic pathways; environmental tolerance; photosynthetic pathways; and nutrient content.

23. (Amended) [A] The nucleic acid molecule of claim 21, wherein the agronomically-significant characteristic is selected from the group consisting of: fruit ripening; oil biosynthesis; pigment biosynthesis; seed formation; starch metabolism; salt tolerance; cold/frost tolerance; drought tolerance; tolerance to anaerobic conditions; protein content; carbohydrate content (including sugars and starches); amino acid content; and fatty acid content.

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25. (Amended) [A] The plant of claim 17, which plant is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; cabbage; oat; rye; cotton; flax; potato; pine; walnut; citrus [(including oranges, grapefruit, etc.)]; hemp; oak; rice; petunia; orchids; Arabidopsis; broccoli; cauliflower; brussel sprouts; onion; garlic; leek; squash; pumpkin; celery; pea; bean [(including various legumes)]; strawberries; grapes; apples; pears; peaches; banana; palm; cocoa; cucumber; pineapple; apricot; plum; sugar beet; lawn grasses; maple; triticale; safflower; peanut; and olive.